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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/943,851A

DATE: 11/29/2001

TIME: 14:17:26

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Output Set: N:\CRF3\11292001\I943851A.raw

1 <110> APPLICANT: Baker, Kevin
 2 Botstein, David
 3 Eaton, Dan
 4 Ferrara, Napoleone
 5 Filvaroff, Ellen
 6 Gerritsen, Mary
 7 Goddard, Audrey
 8 Godowski, Paul
 9 Grimaldi, Christopher
 10 Gurney, Austin
 11 Hillan, Kenneth
 12 Kljavin, Ivar
 13 Napier, Mary
 14 Roy, Margaret
 15 Tumas, Daniel
 16 Wood, William
 17 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 18 ACIDS ENCODING THE SAME
 19 <130> FILE REFERENCE: P2548P1C1
 20 <140> CURRENT APPLICATION NUMBER: 09/943,851A
 21 <141> CURRENT FILING DATE: 2001-08-30
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 23 <151> PRIOR FILING DATE: 2001-05-25
 24 <150> PRIOR APPLICATION NUMBER: 60/067,411
 25 <151> PRIOR FILING DATE: 1997-12-03
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82 <150> PRIOR APPLICATION NUMBER: PCT/US00/03565
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103 <213> ORGANISM: Homo Sapien

104 <400> SEQUENCE: 1

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107      ctcatctttt cttcttacac agtgtctgag aacattttaca ttatagataa 150
108      gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
109      cagtcttaga ctggtcttct acactaagac accatgaagg agtatgtgct 250
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111      acatcgcaat gaagaatatg atgctgaagg atatggaaga cacagatgat 350
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113      tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
114      tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
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116      tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
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118      attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
119      gtcccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
120      cagaactcag aattcatgaa aataaagtta agaaaatata aaaggacaca 800
121      ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaacctct 850
122      tgataataat gggatagagc caggggcatt tgaaggggtg acgggtgttc 900
123      atatcagaat tgcagaagca aaactgacct cagttcctaa aggcttacca 950
124      ccaactttat tggagcttca cttagattat aataaaattt caacagtgga 1000
125      acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
126      acaacaaaat cacagatatc gaaaatggga gtcttgctaa cataccacgt 1100
127      gtgagagaaa tacatttgga aaacaataaa ctaaaaaaa tcccttcagg 1150
128      attaccagag ttgaaatacc tccagataat ctctcttcac tctaattcaa 1200
129      ttgcaagagt gggagtaaat gacttctgtc caacagtgcc aaagatgaag 1250
130      aaatctttat acagtgcaat aagtttatto aacaaccggg tgaaatactg 1300
131      ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350
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136      gatacataag gggttgagag aaacaagcat ctattgcagt ttcttttttg 1600
137      cgtacaaatg atcttacata aatctcatgc ttgaccattc ctttcttcac 1650
138      aacaaaaaag taagatatct ggtatttaac actttgttat caagcacatt 1700
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143      cttatcatgt cttagagccc gtctttatgt ttaaaaactaa tttcttaaaa 1950
144      taaagccttc agtaaatggt cattaccaac ttgataaatg ctactcataa 2000
145      gagctggttt ggggctatag catatgcttt ttttttttta attattacct 2050
146      gatttaaaaa tctctgtaaa aacgtgtagt gtttcataaa atctgtaact 2100

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147      cgcatttttaa tgatccgcta ttataagctt ttaatagcat gaaaattggt 2150
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149      cctttggaag acottgcttg gaagagcctg gacactaaca attctacacc 2250
150      aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
151      tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350
152      gctctatata aatgctcaga gttctttatg tatttcttat tggcattcaa 2400
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164      20 25 30
165      Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
166      35 40 45
167      Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
168      50 55 60
169      Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
170      65 70 75
171      Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
172      80 85 90
173      Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
174      95 100 105
175      Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
176      110 115 120
177      Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
178      125 130 135
179      Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
180      140 145 150
181      Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
182      155 160 165
183      Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
184      170 175 180
185      Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
186      185 190 195
187      Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
188      200 205 210
189      Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
190      215 220 225
191      Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
192      230 235 240
193      Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
194      245 250 255
195      Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
196      260 265 270

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198                      275                      280                      285
199      Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
200                      290                      295                      300
201      Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
202                      305                      310                      315
203      Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
204                      320                      325                      330
205      Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
206                      335                      340                      345
207      Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
208                      350                      355                      360
209      Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
210                      365                      370                      375
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214 <211> LENGTH: 20
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
219 <400> SEQUENCE: 3
220      ggaaatgagt gcaaaccctc 20
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224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
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232 <211> LENGTH: 50
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
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242 <212> TYPE: DNA
243 <213> ORGANISM: Homo Sapien
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247      cctccctccc tctcccccag ctgtcccgtt cgcgtcatgc cgagcctccc 150
248      ggccccgcgc gccccgctgc tgctcctcgc gctgctgctg ctgggctccc 200
249      ggccggcccc cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250

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